

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/807,867

DATE: 08/30/2001
TIME: 11:43:34

Input Set : A:\ES.txt
Output Set: N:\CRF3\08302001\I807867.raw

85 <400> SEQUENCE: 2
87 Met Ala Ala Ile Ser Gly Ile Ser Ser Gly Thr Leu Thr Ile Ser Arg
88 1 5 10 15
88 Pro Leu Val Thr Leu Arg Arg Ser Arg Ala Ala Val Ser Tyr Ser Ser
90 20 25 30
91 Ser His Arg Leu Leu His His Leu Pro Leu Ser Ser Arg Arg Leu Leu
93 35 40 45
94 Leu Arg Asn Asn His Arg Val Gln Ala Thr Ile Leu Gln Asp Asp Glu
96 50 55 60
97 Glu Lys Val Val Val Glu Glu Ser Phe Lys Ala Glu Thr Ser Thr Gly
99 65 70 75 80
100 Thr Glu Pro Leu Glu Glu Pro Asn Met Ser Ser Ser Ser Thr Ser Ala
102 85 90 95
103 Phe Glu Thr Trp Ile Ile Lys Leu Glu Gln Gly Val Asn Val Phe Leu
105 100 105 110
106 Thr Asp Ser Val Ile Lys Ile Leu Asp Thr Leu Tyr Arg Asp Arg Thr
108 115 120 125
109 Tyr Ala Arg Phe Phe Val Leu Glu Thr Ile Ala Arg Val Pro Tyr Phe
111 130 135 140
112 Ala Phe Met Ser Val Leu His Met Tyr Glu Thr Phe Gly Trp Trp Arg
114 145 150 155 160
115 Arg Ala Asp Tyr Leu Lys Val His Phe Ala Glu Ser Trp Asn Glu Met
117 165 170 175
118 His His Leu Leu Ile Met Glu Glu Leu Gly Gly Asn Ser Trp Trp Phe
120 180 185 190
121 Asp Arg Phe Leu Ala Gln His Ile Ala Thr Phe Tyr Tyr Phe Met Thr
123 195 200 205
124 Val Phe Leu Tyr Ile Leu Ser Pro Arg Met Ala Tyr His Phe Ser Glu
126 210 215 220
127 Cys Val Glu Ser His Ala Tyr Glu Thr Tyr Asp Lys Phe Leu Lys Ala
129 225 230 235 240
130 Ser Gly Glu Glu Leu Lys Asn Met Pro Ala Pro Asp Ile Ala Val Lys
132 245 250 255
133 Tyr Tyr Thr Gly Gly Asp Leu Tyr Leu Phe Asp Glu Phe Gln Thr Ser
135 260 265 270
136 Arg Thr Pro Asn Thr Arg Arg Pro Val Ile Glu Asn Leu Tyr Asp Val
138 275 280 285
139 Phe Val Asn Ile Arg Asp Asp Glu Ala Glu His Cys Lys Thr Met Arg
141 290 295 300
142 Ala Cys Gln Thr Leu Gly Ser Leu Arg Ser Pro His Ser Ile Leu Asp
144 305 310 315 320
145 Asp Asp Asp Thr Glu Glu Glu Ser Gly Cys Val Val Pro Glu Glu Ala
147 325 330 335
148 His Cys Glu Gly Ile Val Asp Cys Leu Lys Lys Ser Ile Thr Ser
150 340 345 350
151
153 <210> SEQ ID NO: 3
154 <211> LENGTH: 1387
155 <212> TYPE: DNA
156 <213> ORGANISM: capsicum

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158 <400> SEQUENCE: 3
 159 ccacgcgtcc gataaaaaaa tcaagaatgg cgattccat atctgctatg agttttcgaa 60
 161 cttcagttt ttcttcatat tcagcatttt tgcattttt caagaaccca ttttggggta 120
 163 attctctatt ttcaactttagg aatttcata gaactttca gccttcgtta tcaaggaaat 180
 165 caagtagagt tcgagcaacg ttgttaaaag agaatgaaga agaagtgggt gtggagaaat 240
 167 ctttgcacc taagagttt cctggtaatg tgggggggg aaataatggg gagccacccg 300
 169 ataattcatc ctcgaacggt ctggagaaat gggttataaa gattgagcag tctgtaaata 360
 171 tctttctcac ggattcagtg ataaagattt ttgacactt gtatcacgac cgacactatg 420
 173 cgaggtttt cgttctggaa acaattgcaa gagttcctta tttgcattt atatctgttc 480
 175 ttcacttgcgta cgagagctt gttttttttt gacgacgaga ttatctgaag gtgcattttg 540
 177 ccgagagctg gaatgagatg caccatattac tcattatggg gaaatttagt ggaaatgctt 600
 179 gtttttttgcgatccctt ggcacacata ttgctgtattt ctattattt atgacagtct 660
 181 cgatgtatgc tttttttttt gaaatggcat atcatttctc tgaatgtgt gggccacccatg 720
 183 catacgagac ttacgataaa ttcatcaagg atcaagaagc ggaattgaag aaattgcccgg 780
 185 ctccaaagat tgcagtggc tactacacccg gaggtgactt gtatgttgc gatgagttt 840
 187 aaacatcactc agagcctaactc tcgttgcggc caaaaataga taatctgtac gacgtattca 900
 189 tgaacatcactc agatgacgaa gcaagacattt gtaagacaat gaaagcgtgt caaacccatg 960
 191 ggagcctcg ctccctcac acaaattccat gcaatggcattt tgaagacgat ccagttgtt 1020
 193 cagtcgttca ggccgattttt gtaggtatcg tggattgtat aacgaaatct gtcgtgtatc 1080
 195 ctaacgttcc cagaaggtag gggaaaggaaa aacgcagaac gaaactatac atgtatatac 1140
 197 cagtcgttcc aatatacataa gaaatatacata tacatattgtt atctttact ctctgaggaa 1200
 199 gagctgtca aattgcccggaaaatgggta ggcacttgggt tttgtttca ccttcaata 1260
 201 atttgtacta aactatgaac aaatttgcgcggcacta caactccata ggggtcctgt 1320
 203 tacgcttcgt aactaaattt taacatattt ttgtcaacct tctcagcaaa aaaaaaaaaaa 1380
 205 aaaaaaaaaaa 1387
 208 <210> SEQ ID NO: 4
 209 <211> LENGTH: 357
 210 <212> TYPE: PRT
 211 <213> ORGANISM: capsicum
 213 <400> SEQUENCE: 4
 215 Met Ala Ile Ser Ile Ser Ala Met Ser Phe Arg Thr Ser Val Ser Ser 15
 216 1 5 10 15
 218 Ser Tyr Ser Ala Phe Leu Cys Asn Ser Lys Asn Pro Phe Cys Leu Asn 20 25 30
 219 20 25 30
 221 Ser Leu Phe Ser Leu Arg Asn Ser His Arg Thr Phe Gln Pro Ser Leu 35 40 45
 222 35 40 45
 224 Ser Arg Lys Ser Ser Arg Val Arg Ala Thr Leu Leu Lys Glu Asn Glu 50 55 60
 225 50 55 60
 227 Glu Glu Val Val Val Glu Lys Ser Phe Ala Pro Lys Ser Phe Pro Gly 65 70 75 80
 228 65 70 75 80
 230 Asn Val Gly Gly Asn Asn Gly Glu Pro Pro Asp Asn Ser Ser Ser 85 90 95
 231 85 90 95
 233 Asn Gly Leu Glu Lys Trp Val Ile Lys Ile Glu Gln Ser Val Asn Ile 100 105 110
 234 100 105 110
 236 Phe Leu Thr Asp Ser Val Ile Lys Ile Leu Asp Thr Leu Tyr His Asp 115 120 125
 237 115 120 125
 239 Arg His Tyr Ala Arg Phe Phe Val Leu Glu Thr Ile Ala Arg Val Pro 130 135 140
 240 130 135 140
 242 Tyr Phe Ala Phe Ile Ser Val Leu His Leu Tyr Glu Ser Phe Gly Trp

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243	145	150	155	160
245	Trp Arg Arg Ala Asp Tyr Leu Lys Val His Phe Ala Glu Ser Trp Asn			
246	165	170	175	
248	Glu Met His His Leu Leu Ile Met Glu Glu Leu Gly Gly Asn Ala Trp			
249	180	185	190	
251	Trp Phe Asp Arg Phe Leu Ala Gln His Ile Ala Val Phe Tyr Tyr Phe			
252	195	200	205	
254	Met Thr Val Ser Met Tyr Ala Leu Ser Pro Arg Met Ala Tyr His Phe			
255	210	215	220	
257	Ser Glu Cys Val Glu His His Ala Tyr Glu Thr Tyr Asp Lys Phe Ile			
258	225	230	235	240
260	Lys Asp Gln Glu Ala Glu Leu Lys Lys Leu Pro Ala Pro Lys Ile Ala			
261	245	250	255	
263	Val Ser Tyr Tyr Thr Gly Gly Asp Leu Tyr Leu Phe Asp Glu Phe Gln			
264	260	265	270	
266	Thr Ser Arg Glu Pro Asn Thr Arg Arg Pro Lys Ile Asp Asn Leu Tyr			
267	275	280	285	
269	Asp Val Phe Met Asn Ile Arg Asp Asp Glu Ala Glu His Cys Lys Thr			
270	290	295	300	
272	Met Lys Ala Cys Gln Thr His Gly Ser Leu Arg Ser Pro His Thr Asn			
273	305	310	315	320
275	Pro Cys Asp Glu Ser Glu Asp Asp Pro Gly Cys Ser Val Pro Gln Ala			
276	325	330	335	
278	Asp Cys Val Gly Ile Val Asp Cys Ile Thr Lys Ser Val Ala Asp Pro			
279	340	345	350	
281	Asn Val Gly Arg Arg			
282	355			
284	<210> SEQ ID NO: 5			
285	<211> LENGTH: 1284			
286	<212> TYPE: DNA			
287	<213> ORGANISM: tomato			
289	<400> SEQUENCE: 5			
290	gaattcggca cgagcggcac gagcagaaaa ctaacaactt tcccaacttg gaattttctt		60	
292	taccttacct aagaaggta ttaatttgat tcttgggga aggaagaagg atcaagaatg		120	
294	gcgatttcga tttctgctat gagtttgga acctcagttt cttcatattc ttgtttttaga		180	
296	gctaggagtt ttgagaagtc atcagttta tgcaattccc agaaccatg tcggtttaat		240	
298	tctgttttc cgattcggaa atctgatggg gcttcacggt gttctgttc tagaaatca		300	
300	tgttaggttc gagcaacgtt gttacaagag aatgaagaag aagtggtgt ggagaaatct		360	
302	tttgcaccta agagtttcc tgataacgtg ggagggggaa gtaatgggaa gccaccagat		420	
304	gattcatctt ctaacggct agagaaatgg gttataaagc ttgagcagtc tgtaaatatc		480	
306	ttactcacgg attcagtgtt aaagattctt gacactttgt atcacaaccc aaactatgcg		540	
308	aggttttttg ttctggaaac aattgcaagg gttccttatt ttgcatttat atcggttctt		600	
310	cacatgtatg agagcttgg ctggtgaga agggcagatt atatgaaagt gcattttgc		660	
312	gaaagctgga atgagatgca ccatttgcattatggaa aatttagggg aaatgcttgg		720	
314	tggtttgatc gatttcttgc acaacatata gctatattct attatttcat gacagtctt		780	
316	atgtatgctt tgagcccgag aatggcatat catttctctg aatgtgtgg aagccatgca		840	
318	tacgagactt acgataaatt catcaaggat caaggagagg aattgaagaa ttgcccgc		900	
320	ccaaagattg cagtggacta ctacacggg ggtgacttat atttatttga tgagtttcaa		960	
322	acttcacgag agcctaatac tcgaagacca aaaatagata atctctatga cgtattcatg		1020	

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324 aacatttagag atgacgaagc agagcattgt aaaacgatga aagcctgtca aactcacggg 1080
 326 agccttcgtt ctcccacac agatccatgc gatgattctg aagatgatac agggtgttcc 1140
 328 gtacctaag ctgattgtat aggtatcgtg gattgtataa agaagtcagt caccgatact 1200
 330 caagtaacca aaaggtagga aaaggaaaaa cgccgacaaa ctatacttgt atataactagt 1260
 332 atagacaaaa aaaaaaaaaa aaaa 1284
 335 <210> SEQ ID NO: 6
 336 <211> LENGTH: 19
 337 <212> TYPE: DNA
 C--> 338 <213> ORGANISM: Artificial
 340 <220> FEATURE:
 341 <223> OTHER INFORMATION: PCR primer ✓
 343 <400> SEQUENCE: 6
 344 gcaacgatt tgcaagacg 19
 347 <210> SEQ ID NO: 7
 348 <211> LENGTH: 24
 349 <212> TYPE: DNA
 C--> 350 <213> ORGANISM: Artificial
 352 <220> FEATURE:
 353 <223> OTHER INFORMATION: PCR primer ✓
 355 <400> SEQUENCE: 7 24
 356 ttaacttgtatggattct tgag
 359 <210> SEQ ID NO: 8
 360 <211> LENGTH: 171
 361 <212> TYPE: PRT
 362 <213> ORGANISM: soybean
 364 <400> SEQUENCE: 8
 366 Tyr Arg Thr Val Lys Leu Leu Arg Ile Pro Thr Asp Leu Phe Phe Lys
 367 1 5 10 15
 369 Arg Arg Tyr Gly Cys Arg Ala Met Met Leu Glu Thr Val Ala Ala Val
 370 20 25 30
 372 Pro Gly Met Val Gly Gly Met Leu Leu His Leu Arg Ser Leu Arg Lys
 373 35 40 45
 375 Phe Gln Gln Ser Gly Gly Trp Ile Lys Ala Leu Leu Glu Glu Ala Glu
 376 50 55 60
 378 Asn Glu Arg Met His Leu Met Thr Met Val Glu Leu Val Lys Pro Lys
 379 65 70 75 80
 381 Trp Tyr Glu Arg Leu Leu Val Leu Ala Val Gln Gly Val Phe Phe Asn
 382 85 90 95
 384 Ala Phe Phe Val Leu Tyr Ile Leu Ser Pro Lys Val Ala His Arg Ile
 385 100 105 110
 387 Val Gly Tyr Leu Glu Glu Ala Ile His Ser Tyr Thr Glu Tyr Leu
 388 115 120 125
 390 Lys Asp Leu Glu Ser Gly Ala Ile Glu Asn Val Pro Ala Pro Ala Ile
 391 130 135 140
 393 Ala Ile Asp Tyr Trp Arg Leu Pro Lys Asp Ala Arg Leu Lys Asp Val
 394 145 150 155 160
 396 Ile Thr Val Ile Arg Ala Asp Glu Ala His His
 397 165 170
 399 <210> SEQ ID NO: 9

VERIFICATION SUMMARY
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Output Set: N:\CRF3\08302001\I807867.raw

L:338 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:350 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7